

Amendments to the Claims

Claims 1-60 (Cancelled).

Claim 61 (New): A method for identifying a pig with a polymorphism at position 89 of SEQ ID NO:1 wherein a pig with a cytosine at position 89 of SEQ ID NO:3 is indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with adenosine at position 89 of SEQ ID NO:1 wherein the polymorphism is indicative of meat quality traits comprising:
detecting the nucleotide present at position 89 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 62 (New): The method of claim 1 wherein the polymorphism is detected at position 89 of a PCR sequence using a forward primer and a reverse primer.

Claim 63 (New): The method of claim 1 wherein the step of detecting the polymorphism is a method employing allele specific primers.

Claim 64 (New): The method of claim 2 wherein said forward primer has an oligonucleotide sequence 5'ATG AGC TTC CTA GAG CAA GGA G 3' (SEQ ID NO:13) and said reverse primer has an oligonucleotide sequence 5'GGC TGC ATG ATG TTA TGT GCC T 3' (SEQ ID NO:14).

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Claim 65 (New): The method of claim 1 wherein the step of detecting the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and temperature gradient gel electrophoresis (TGGE).

Claim 66 (New): The method of claim 5 further comprising the step of amplifying SEQ ID NO:3 or a region of thereof containing said polymorphism.

Claim 67 (New): The method of claim 6 further comprising the step of digesting the amplified region with the restriction endonuclease *SpyI*.

Claim 68. The method of claim 7 wherein said polymorphism is a 198 and 72 base pairs (bp) restriction length polymorphism.

Claim 69 (New): The method of claim 7 wherein said polymorphism is a 198 bp, 181 bp, 72 bp and 17 bp restriction length polymorphism.

Claim 70 (New): The method of claim 7 wherein said polymorphism is a 181 bp, 72 bp and 17 bp restriction length polymorphism.

Claim 71 (New): A method for identifying a pig with a polymorphism at position 154 of SEQ ID NO:3 wherein a pig with an adenosine at position 154 of SEQ ID NO:3 is indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with

guanine at position 154 of SEQ ID NO:3 wherein the polymorphism is indicative of meat quality traits comprising:

detecting the nucleotide present at position 154 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 72 (New): The method of claim 11 wherein the polymorphism is detected at position 154 of a PCR sequence using a forward primer and a reverse primer.

Claim 73 (New): The method of claim 11 wherein the step of detecting the polymorphism is a method employing allele specific primers.

Claim 74 (New): The method of claim 12 wherein said forward primer has an oligonucleotide sequence 5'ATG AGC TTC CTA GAG CAA GGA G 3' (SEQ ID NO:13) and said reverse primer has an oligonucleotide sequence 5'GGC TGC ATG ATG TTA TGT GCC T 3' (SEQ ID NO:14).

Claim 75 (New): The method of claim 1 wherein the step of detecting the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and temperature gradient gel electrophoresis (TGGE).

Claim 76 (New): The method of claim 15 further comprising the step of amplifying SEQ ID NO:3 or a region of thereof containing said polymorphism.

Claim 77 (New): The method of claim 16 further comprising the step of digesting the amplified region with the restriction endonuclease *HphI*.

Claim 78 (New): The method of claim 17 wherein said polymorphism is a 270 base pairs (bp) restriction length polymorphism.

Claim 79 (New): The method of claim 17 wherein said polymorphism is a 270 bp, 158 bp and 112 bp restriction length polymorphism.

Claim 80 (New): The method of claim 17 wherein said polymorphism is a 158 bp and 112 bp restriction length polymorphism.

Claim 81 (New): A method for identifying a pig with a polymorphism at position 595 of SEQ ID NO:3 wherein a pig with a adenosine at position 595 of SEQ ID NO:3 is indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with guanine at position 595 of SEQ ID NO:3 wherein the polymorphism is indicative of meat quality traits comprising:
detecting the nucleotide present at position 595 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 82 (New): The method of claim 21 wherein the polymorphism is detected at position 595 of a PCR sequence using a forward primer and a reverse primer.

Claim 83 (New): The method of claim 21 wherein the step of detecting the polymorphism is a method employing allele specific primers.

Claim 84 (New): The method of claim 22 wherein said forward primer has an oligonucleotide sequence 5'GGA GCA AAT GTG CAG ACA AG 3' (SEQ ID NO:16) and said reverse primer has an oligonucleotide sequence 5'CCC ACG AAG CTC TGC TTC TT 3' (SEQ ID NO:17).

Claim 85 (New): The method of claim 1 wherein the step of detecting the polymorphism is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and temperature gradient gel electrophoresis (TGGE).

Claim 86 (New): The method of claim 25 further comprising the step of amplifying SEQ ID NO:3 or a region of thereof containing said polymorphism.

Claim 87 (New): The method of claim 26 further comprising the step of digesting the amplified region with the restriction endonuclease *Bsa*Hi.

Claim 88 (New): The method of claim 27 wherein said polymorphism is a 167 bp and 91 bp restriction length polymorphism.

Claim 89 (New): The method of claim 27 wherein said polymorphism is a 167 bp, 119 bp and 91 bp restriction length polymorphism.

Claim 90 (New): The method of claim 27 wherein said polymorphism is a 119 bp and 91 bp restriction length polymorphism.

Claim 91 (New): A method for identifying a pig with polymorphisms at position 595 of SEQ ID NO:3 wherein a pig with an adenosine at position 595 of SEQ ID NO:3 and a codon at positions 598-600 of SEQ ID NO:3 encoding Arg are indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with a guanine at position 595 of SEQ ID NO:3 and a codon at positions 598-600 of SEQ ID NO:3 encoding Arg wherein the polymorphism and the codon at positions 598-601 of SEQ ID NO:3 encoding for Arg are indicative of meat quality traits comprising:
detecting the nucleotide present at position 595 of SEQ ID NO: 3; and
detecting the codon present at positions 598-600 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 92 (New): A method for identifying a pig with polymorphisms at position 89 of SEQ ID NO:3, at position 154 of SEQ ID NO:3, and at position 595 of SEQ ID NO:3 wherein a pig with a cytosine at position 89, an adenosine at position 154, an adenosine at position 595 and a codon at positions 598-600 of SEQ ID NO:3 encoding Arg are indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with adenosine at position 89 of SEQ ID NO:3, a guanine at position 154 of SEQ ID NO:3, a guanine at position 595 of

SEQ ID NO:3, and a codon at positions 598-600 of SEQ ID NO:3 encoding Arg, wherein the polymorphisms and the codon at positions 598-600 encoding Arg are indicative of meat quality traits comprising:

detecting the nucleotide present at position 89 of SEQ ID NO: 3; and
detecting the nucleotide present at position 154 of SEQ ID NO: 3; and
detecting the nucleotide present at position 595 of SEQ ID NO: 3; and
detecting the codon present at position 598-600 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 93 (New): A method for identifying a pig with polymorphisms at position 89 of SEQ ID NO:3, at position 154 of SEQ ID NO:3, at position 595 of SEQ ID NO:3, wherein a pig with a cytosine at position 89, a codon at positions 154-156 of SEQ ID NO:3 encoding Ile, and an adenosine at position 595 of SEQ ID NO:3 are indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with adenosine at position 89 of SEQ ID NO:3, a codon at positions 154-156 of SEQ ID NO:3 encoding Gly, a guanine at position 595 of SEQ ID NO:3, wherein the polymorphisms and the codon at positions 154-156 encoding Ile, are indicative of meat quality traits comprising:

detecting the nucleotide present at position 89 of SEQ ID NO: 3; and
detecting the codon present at position 154-156 of SEQ ID NO: 3; and
detecting the nucleotide present at position 595 of SEQ ID NO: 3; and
relating the polymorphism to the phenotype.

Claim 94 (New): A method for identifying a pig with polymorphisms at position 89 of SEQ ID NO:3, at position 154 of SEQ ID NO:3, at position 595 of SEQ ID NO:3, wherein a pig with a cytosine at position 89 of SEQ ID NO:3, a codon at positions 154-156 of SEQ ID NO:3 encoding Ser, a guanine at position 595 of SEQ ID NO:3 are indicative of said pig more likely to have higher ham and loin pH and ham and loin Minolta than a pig with an adenosine at position 89 of SEQ ID NO:3, a codon at positions 154-156 of SEQ ID NO:3 encoding Gly, and a guanine at position 595 of SEQ ID NO:3, wherein a cytosine at position 89, a codon at positions 154-156 encoding Ser, and a guanine at position 595 are indicative of meat quality traits comprising: detecting the nucleotide present at position 89 of SEQ ID NO: 3; and detecting the codon present at position 154-156 of SEQ ID NO: 3; and detecting the nucleotide present at position 595 of SEQ ID NO: 3; and relating the polymorphism to the phenotype.

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